

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (currently amended) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a ~~fungus~~ **Phytophthora** comprising:

(a) constructing a library of peptides by,

(i) preparing random oligonucleotides;

(ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;

(iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;

(b) contacting said vector expressing said peptide library with a target ~~fungus~~ **Phytophthora** and removing unbound vector, wherein the target **Phytophthora** is selected from the group consisting of **Phytophthora sojae**, **Phytophthora capsici**, **Phytophthora palmivora**, **Phytophthora cinnamomi**, and **Phytophthora parasitica**;

(c) eluting bound vector from said ~~fungus~~ **Phytophthora**;

(d) amplifying said bound vector;

(e) sequencing the oligonucleotides contained in said eluted vector;

(f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and

(g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

2. (original) The method of claim 1, further comprising repeating steps (b) through (d) at least once.

3. (original) The method of claim 1, wherein said vector is a fusion phage vector.
4. (original) The method of claim 1, wherein said vector is a fusion phage vector selected from the group consisting of type 8, type 88, type 8+8, type 3, type 33, type 3+3, type 6, type 66, type 6+6, phage T7 and phage 8.
5. (original) The method of claim 1, wherein the sequence of said random oligonucleotide is GCA GNN (NNN)₇ or SEQ ID NO: 1.
6. (original) The method of claim 1, wherein said peptide is expressed as part of a coat protein of said vector.
7. (original) The method of claim 6, wherein said coat protein is a pIII or a pVIII coat protein.
8. (currently amended) The method of claim 1, further comprising determining the binding affinity of said peptides to said target **fungus Phytophthora**.
9. (previously presented) The method of claim 1, wherein each of said peptides are of the same length, the length being 6 to 15 amino acids.
- 10-35. (canceled)
36. (currently amended) The method of claim 1 wherein the target **fungus Phytophthora** is *Phytophthora sojae* or *Phytophthora capsici*.
37. (currently amended) The method of claim 1 wherein the vector expressing the peptide library is contacted with the target **fungus Phytophthora** at different life stages of the target fungus.

38. (currently amended) The method of claim 1 wherein the vector expressing the peptide library is contacted with the target **fungus Phytophthora** at oospore life stage or chlamydospore life stage.

39. (currently amended) The method of claim 1 wherein the vector expressing the peptide library is contacted with the target **fungus Phytophthora** at zoospore life stage.

40. (currently amended) The method of claim 1 wherein the vector expressing the peptide library is contacted with the target **fungus Phytophthora** at germling life stage.

41. (previously presented) The method of claim 1 wherein each of said peptides are of a same length, the length being 8 amino acids.

42. (previously presented) The method of claim 41 wherein the peptide library is an f8-1 peptide library.

43. (previously presented) The method of claim 1 wherein each of said peptides are of a same length, the length being 15 amino acids.

44. (previously presented) The method of claim 43 wherein the peptide library is an f88-4 peptide library.

45. (previously presented) The method of claim 1, further comprising repeating steps (b) through (d) at least twice.

46. (previously presented) The method of claim 1, further comprising repeating steps (b) through (d) at least three times.

47. (previously presented) The method of claim 1 wherein the bound vector is amplified in an *E. coli*.

48. (new) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus comprising:

- (a) constructing a library of peptides by,
 - (i) preparing random oligonucleotides;
 - (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;
 - (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;wherein each of said peptides are of a same length, the length being 8 amino acids, and the peptide library is an f8-1 peptide library;
- (b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;
- (c) eluting bound vector from said fungus;
- (d) amplifying said bound vector;
- (e) sequencing the oligonucleotides contained in said eluted vector;
- (f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and
- (g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

49. (new) The method of claim 48, further comprising repeating steps (b) through (d) at least once.

50. (new) The method of claim 49, further comprising repeating steps (b) through (d) at least twice.

51. (new) The method of claim 48, wherein said vector is a fusion phage vector.

52. (new) The method of claim 51, wherein said vector is a fusion phage vector selected from the group consisting of type 8, type 88, type 8+8, type 3, type 33, type 3+3, type 6, type 66, type 6+6, phage T7 and phage 8.

53. (new) The method of claim 48, wherein said peptide is expressed as part of a coat protein of said vector.

54. (new) The method of claim 53, wherein said coat protein is a pIII or a pVIII coat protein.

55. (new) The method of claim 48, further comprising determining the binding affinity of said peptides to said target fungus.

56. (new) The method of claim 48 wherein the target fungus is a *Phytophthora*.

57. (new) The method of claim 56 wherein the target *Phytophthora* is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora cactorum*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, *Phytophthora infestans*, and *Phytophthora parasitica*.

58. (new) The method of claim 57 wherein the target *Phytophthora* is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.

59. (new) The method of claim 58 wherein the target *Phytophthora* is *Phytophthora sojae* or *Phytophthora capsici*.

60. (new) The method of claim 48 wherein the vector expressing the peptide library is contacted with the target fungus at a different life stage of the target fungus

selected from the group consisting of oospore life stage, chlamydospore life stage, zoospore life stage, and germling life stage.

61. (new) A method for identification of non-immunoglobulin peptides having an affinity for the surface of a fungus comprising:

- (a) constructing a library of peptides by,
 - (i) preparing random oligonucleotides;
 - (ii) inserting said oligonucleotides into a vector that expresses peptides encoded by said random oligonucleotides on its surface and is capable of transfecting a host cell;
 - (iii) transfecting a host cell with said vector to amplify said vector in an infectious form to create a library of peptides on the surface of said vector;
wherein each of said peptides are of a same length, the length being 15 amino acids, and the peptide library is an f88-4 peptide library;
- (b) contacting said vector expressing said peptide library with a target fungus and removing unbound vector;
- (c) eluting bound vector from said fungus;
- (d) amplifying said bound vector;
- (e) sequencing the oligonucleotides contained in said eluted vector;
- (f) deducing the amino acid sequence of peptides encoded by said oligonucleotides contained in said eluted vector; and
- (g) selecting the non-immunoglobulin peptides for which the amino acid sequence has been deduced.

62. (new) The method of claim 61, further comprising repeating steps (b) through (d) at least once.

63. (new) The method of claim 62, further comprising repeating steps (b) through (d) at least twice.

64. (new) The method of claim 61, wherein said vector is a fusion phage vector.

65. (new) The method of claim 64, wherein said vector is a fusion phage vector selected from the group consisting of type 8, type 88, type 8+8, type 3, type 33, type 3+3, type 6, type 66, type 6+6, phage T7 and phage 8.

66. (new) The method of claim 61, wherein said peptide is expressed as part of a coat protein of said vector.

67. (new) The method of claim 66, wherein said coat protein is a pIII or a pVIII coat protein.

68. (new) The method of claim 61, further comprising determining the binding affinity of said peptides to said target fungus.

69. (new) The method of claim 61 wherein the target fungus is a *Phytophthora*.

70. (new) The method of claim 69 wherein the target *Phytophthora* is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora cactorum*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, *Phytophthora infestans*, and *Phytophthora parasitica*.

71. (new) The method of claim 70 wherein the target *Phytophthora* is selected from the group consisting of *Phytophthora sojae*, *Phytophthora capsici*, *Phytophthora palmivora*, *Phytophthora cinnamomi*, and *Phytophthora parasitica*.

72. (new) The method of claim 71 wherein the target *Phytophthora* is *Phytophthora sojae* or *Phytophthora capsici*.

73. (new) The method of claim 61 wherein the vector expressing the peptide library is contacted with the target fungus at a different life stage of the target fungus

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selected from the group consisting of oospore life stage, chlamydospore life stage, zoospore life stage, and germling life stage.